

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 30, 2002, 11:50:30 ; Search time 27.34 Seconds  
(without alignments)  
39.007 Million cell updates/sec

Title: US-09-432-546-5  
Perfect score: 103  
Sequence: 1 SRPMPWMPKWLPI 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	62	60.2	144	1	JC1222	indolicidin precursor
2	57	55.3	1662	2	T18540	moA protein precursor
3	56	54.4	236	2	U00806	arylsulfatase (EC 3
4	56	54.4	236	2	F83705	hypothetical prote
5	53.5	51.9	497	1	A40487	ferredoxin-NADP+
6	53	51.5	95	2	E86447	protein FSD14.5 [1
7	52.5	51.0	970	2	C84488	hypothetical prote
8	52.5	51.0	1231	2	C84716	hypothetical prote
9	52	50.5	301	2	G83556	hypothetical prote
10	52	50.5	1112	2	S70522	cyclic nucleotide
11	51.5	50.0	196	2	B48232	cysteine-rich exte
12	51.5	50.0	209	2	A48232	photosynthetic rea
13	51.5	50.0	279	2	S68239	photosynthetic rea
14	51.5	50.0	279	2	E49664	photosynthetic rea
15	51.5	50.0	279	2	T50889	photosynthetic rea
16	51.5	50.0	321	2	F84611	hypothetical prote
17	51.5	50.0	498	1	JT0751	ferredoxin-NADP+
18	51.5	50.0	2970	2	T08839	polyprotein - marm
19	51	49.5	1173	1	VGTHHC	E2 glycoprotein pr
20	50.5	49.0	560	2	T32661	hypothetical prote
21	50	48.5	83	2	B72392	hypothetical prote
22	49.5	48.1	253	2	G70715	hypothetical prote
23	49.5	48.1	257	2	S70177	hypothetical prote
24	49	47.6	169	2	F72532	YifE protein - Yef
25	49	47.6	456	1	I40516	spA protein - Bac
26	49	47.6	669	2	T28028	hypothetical prote
27	48.5	47.1	212	2	S57330	cathepsin-like anti
28	48.5	47.1	228	2	S40463	prophenin (Pr-2) p
29	48	46.6	314	2	H84677	hypothetical prote

30	48	46.6	947	2	H85088	hypothetical prote
31	48	46.6	990	1	G46335	env polyprotein pr
32	48	46.6	1172	2	F96503	protein F9C16.13 l
33	47.5	46.1	111	2	T29295	hypothetical prote
34	47.5	46.1	248	2	S23449	NADH oxidase (H202
35	47.5	46.1	752	2	E82146	Rec2-related prote
36	47	45.6	73	2	D75497	hypothetical prote
37	47	45.6	212	2	PQ0518	envelope protein -
38	47	45.6	233	2	B96552	protein F23N19.5 l
39	47	45.6	253	2	D86310	protein F113.4 [lm
40	47	45.6	299	2	T12505	hypothetical prote
41	47	45.6	964	1	VCLJ06	env polyprotein pr
42	47	45.6	966	1	VCLJ06	env polyprotein pr
43	47	45.6	982	1	VCLJVS	env polyprotein pr
44	47	45.6	983	1	E45390	env polyprotein pr
45	47	45.6	1055	2	A96682	protein F1E22.12 l

## ALIGNMENTS

RESULT 1  
JC1222  
Indolicidin precursor - bovine  
N:Alternate names: antimicrobial peptide  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: JC1222; A42387; S25664  
R:del Sal, G.; Storicl, P.; Schneider, C.; Romeo, D.; Zanetti, M.  
Biochem. Biophys. Res. Commun. 187, 467-472, 1992  
A:Title: cDNA cloning of the neutrophil bactericidal peptide indolicidin.  
A:Reference number: JC1222; MUID:92392368  
A:Accession: JC1222  
A:Molecule type: mRNA  
A:Residues: 1-144 <SAL>  
A:Cross-references: EMBL:X67340; NID:9462; PIDN:CAA47755.1; PID:9463  
A:Experimental source: bone marrow  
J:Seasted, M.E.; Novotny, M.J.; Morris, W.L.; Tang, Y.Q.; Smith, W.; Cullor, J.S.  
J. Biol. Chem. 267, 4292-4295, 1992  
A:Title: Indolicidin, a novel bactericidal tridecapeptide amide from neutrophils.  
A:Reference number: A42387; MUID:92165771  
A:Accession: A42387  
A:Molecule type: protein  
A:Residues: 131-143 <SEL>  
A:Experimental source: neutrophils  
A>Note: sequence extracted from NCBI backbone (NCBI:83840)  
C:Superfamily: cathepsin; cystatin homology  
C:Keywords: amidated carboxyl end  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:22-129/Domain: cystatin homology <CVS>  
F:30-130/Domain: propeptide #status predicted <PRO>  
F:131-143/Product: indolicidin #status experimental <MAT>  
F:143/Modified site: amidated carboxyl end (Arg) (amide in mature form from following

Query Match 60.2% Score 62; DB 1; Length 144;  
Best Local Similarity 75.0%; Pred. No. 0.24;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RWPMPWK 10  
DB 135 KMPMPWR 142

RESULT 2  
T18540  
moA protein precursor [imported] - Leptothrix discophora  
C:Species: Leptothrix discophora  
C:Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 08-Sep-2000  
C:Accession: T18540  
R:Corstjens, P.L.  
submitted to the EMBL Data Library, April 1999  
A:Reference number: Z18959

A:Accession: T18540  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1662 <COR>  
 A:Cross-references: EMBL:225774; NID:e1427784; PID:e267517; PIDN:CAA81037.1  
 C:Genetics:  
 A:Note: mofa  
 F:1-33/Domain: signal sequence #status predicted <Sig>  
 F:43-1662/Product: mofa protein #status predicted <MAT>

Query Match 55.3%; Score 57; DB 2; Length 1662;  
 Best Local Similarity 63.6%; Pred. No. 10;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 RMPMPMPKMP L 13  
 DB 490 RHHMGFWMPV 500

# RESULT 3

J00606  
 arylesterase (EC 3.1.1.2) precursor - Pseudomonas fluorescens  
 C:Species: Pseudomonas fluorescens  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 31-Mar-2000  
 C:Accession: J00606  
 R:Choi, K.D.; Jeon, G.H.; Rhee, J.S.; Yoo, O.J.  
 Agric. Biol. Chem. 54, 2039-2045, 1990  
 A:Title: Cloning and nucleotide sequence of an esterase gene from Pseudomonas fluorescens  
 A:Reference number: J00606; MUID:91182405  
 A:Accession type: DNA  
 A:Residues: 1-236 <CHO>  
 A:Cross-references: GB:D12484; GB:D01134; NID:9216856; PIDN:BA02052.1; PID:dl002534; PI  
 A:Note: Part of this sequence, including the amino end of the mature protein, was confir  
 C:Keywords: carboxylic ester hydrolase  
 F:2-236/Product: arylesterase #status predicted <MAT>

Query Match 54.4%; Score 56; DB 2; Length 236;  
 Best Local Similarity 42.1%; Pred. No. 2.1;  
 Matches 8; Conservative 3; Mismatches 2; Indels 6; Gaps 1;

QY 1 SRRW-----PMWPKMPL 13  
 DB 204 ARTWPRSTYPMYPMKMR L 222

# RESULT 4

F83705  
 hypothetical protein BH0446 [imported] - Bacillus halodurans (strain C-125)  
 C:Species: Bacillus halodurans  
 C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 31-Dec-2000  
 C:Accession: F83705  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A:Reference number: AB3650; MUID:20263314  
 A:Accession: F83705  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-236 <STO>  
 A:Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BA04165.1; GSPDB:GN00  
 C:Experimental source: strain C-125  
 C:Genetics:  
 A:Gene: BH0446

Query Match 54.4%; Score 56; DB 2; Length 236;  
 Best Local Similarity 77.8%; Pred. No. 2.1;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 WMPKMP L 14

DB 192 WLPKMP L 200

# RESULT 5

A40487  
 ferredoxin--NADP+ reductase (EC 1.18.1.2), long form, precursor - human  
 N:Alternate names: adrenodoxin reductase  
 C:Species: Homo sapiens (man)  
 C:Date: 24-Jan-1992 #sequence\_revision 18-Oct-1996 #text\_change 11-Jun-1999  
 C:Accession: A40487; B40487; A36482  
 R:Solish, S.B.; Picado-Leonard, J.; Morel, Y.; Kuhn, R.W.; Mohandas, T.K.; Hanukoglu,  
 Proc. Natl. Acad. Sci. U.S.A. 85, 7104-7108, 1988  
 A:Title: Human adrenodoxin reductase: two mRNAs encoded by a single gene on chromosome  
 A:Reference number: A40487; MUID:89017146  
 A:Accession: A40487

A:Molecule type: mRNA  
 A:Residues: 1-497 <SOL>

A:Cross-references: GB:003826; NID:g178212; PIDN:AAB59498.1; PID:g178214

A:Accession: B40487

A:Molecule type: mRNA  
 A:Residues: 66-122, 'R', 124-203, 210-497 <SO2>

A:Cross-references: GB:003826

R:Lin, D.; Shi, Y.; Miller, W.L.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 8516-8520, 1990

A:Title: Cloning and sequence of the human adrenodoxin reductase gene.

A:Reference number: A36482; MUID:91046028

A:Accession: A36482

A:Molecule type: DNA  
 A:Residues: 1-122, 'R', 124-497 <LIN>

A:Cross-references: GB:M38255; GB:M68509; GB:M38256; NID:g178206; PIDN:AAA5166.1; PI

C:Comment: Ferredoxin--NADP+ reductase is localized in the matrix of adrenal cortex m

ferredoxin--NADP+ reductase, adrenodoxin and two forms of cytochrome P-450.

C:Genetics:

A:Gene: GDB:FDXR; ADXR

A:Cross-references: GDB:119659; OMIM:103270

A:Map position: 17q24-17q25

C:Function:

A:Description: catalyzes the reversible reduction of NADP+ by reduced ferredoxin or r

C:Superfamily: human ferredoxin--NADP+ reductase

C:Keywords: alternative splicing; electron transfer; flavoprotein; mitochondrion; mon

F:1-32/Domain: transit peptide (mitochondrion) #status predicted <Sig>

F:33-497/Product: ferredoxin--NADP+ reductase, long form #status predicted <MAT>

F:33-203, 210-497/Product: ferredoxin--NADP+ reductase, short form #status predicted <

F:40-69/Region: beta-alpha-beta FAD nucleotide-binding fold

F:179-189/Region: NADP binding #status predicted

F:280/Binding site: substrate (Lys) #status predicted

QY 1 SRRMPMPKMP L 12  
 DB 3 SRCWRMGWSAMP 15

# RESULT 6

E86447  
 protein FSD14.5 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: E86447  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
 ansen, N.F.; Hughes, B.; Hultzar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marzia  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: E86447  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-95 <STO>  
A:Cross-references: GB:AE005172; NID:g8920603; PIDN:AAF81325.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F5D14.5  
A:Map position: 1

Query Match 51.5%; Score 53; DB 2; Length 95;  
Best Local Similarity 29.6%; Pred. No. 2.1;  
Matches 8; Conservative 2; Mismatches 3; Indels 14; Gaps 1;

QY 2 RPMPMP-----WKMPPL 14  
||| |||  
DB 59 RNMMMPVLVITDVGEWMSWMMWMPVL 85

RESULT 7  
C84488  
Hypothetical protein At2g07730 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: C84488  
R:Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Molloy, K.S.; Cronin, U.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999  
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: C84488  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-970 <STO>  
A:Cross-references: GB:AE002093; NID:g3327392; PIDN:AAC26674.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g07730  
A:Map position: 2

Query Match 51.0%; Score 52.5; DB 2; Length 970;  
Best Local Similarity 46.7%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 4 WP-----WMPKW 11  
||| |||  
DB 739 WPTLFSGIWMWANKW 753

RESULT 8  
C84716  
Hypothetical protein At2g31080 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: C84716  
R:Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Molloy, K.S.; Cronin, U.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999  
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: C84716  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1231 <STO>  
A:Cross-references: GB:AE002093; NID:g3746069; PIDN:AAC63844.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g31080  
A:Map position: 2

Query Match 51.0%; Score 52.5; DB 2; Length 1231;  
Best Local Similarity 46.7%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 4 WP-----WMPKW 11  
||| |||  
DB 1000 WPTLFSGIWMWANKW 1014

RESULT 9  
G83556  
Hypothetical protein PA0702 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: G83556  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitsuuchi, S.D.; Warren, P.; Hickey, M.J.; Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000  
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.  
A:Reference number: A82950; MUID:20437337  
A:Accession: G83556  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-301 <STO>  
A:Cross-references: GB:AE004506; GB:AE004091; NID:g9946584; PIDN:AAG04091.1; GSPDB:GN00139  
A:Experimental source: Strain PA01  
C:Genetics:  
A:Gene: PA0702

Query Match 50.5%; Score 52; DB 2; Length 301;  
Best Local Similarity 70.0%; Pred. No. 8.3;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 WPMPMPKMPPL 13  
||| |||  
DB 97 WPMWQAMPPL 106

RESULT 10  
S70522  
cyclic nucleotide phosphodiesterase, cGMP-inhibited (EC 3.1.4.-) - human  
C:Species: Homo sapiens (man)  
C>Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 19-May-2000  
C:Accession: S70522  
R:Murata, T.; Taira, M.; Manganiello, V.C. FEBS Lett. 390, 29-33, 1996  
A>Title: Differential expression of cGMP-inhibited cyclic nucleotide phosphodiesterases.  
A:Reference number: S70522; MUID:96314543  
A:Accession: S70522  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-1112 <MUR>  
A:Cross-references: EMBL:U038178; NID:g1145301; PIDN:AAC50724.1; PID:g1145302  
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, January 1996  
C:Keywords: phosphoric diester hydrolase  
F:736-1006/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 50.5%; Score 52; DB 2; Length 1112;  
Best Local Similarity 62.5%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 WPMPMPKW 11  
||| |||  
DB 169 WQWMPMPW 176

RESULT 11  
B48232

cysteine-rich extensin-like protein 2 precursor - common tobacco  
 C:Species: Nicotiana tabacum (common tobacco)  
 C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 01-Dec-2000  
 C:Accession: B48232; PQ0474; S24616  
 R:Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993  
 A:Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain  
 A:Reference number: A48232; MUID:93342083  
 A:Accession: B48232  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-196 <WUA>  
 A:Cross-references: GB:L13440; NID:g310924; PIDN:AAA34060.1; PID:g310925  
 R:de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.  
 Plant Cell 4, 1041-1051, 1992  
 A:Title: Developmental expression of tobacco pistil-specific genes encoding novel extensin  
 A:Reference number: PQ0474; MUID:93005740  
 A:Accession: PQ0474  
 A:Molecule type: mRNA  
 A:Residues: 'MAG', 1-105 <GOL>  
 A:Cross-references: EMBL:Z14014  
 A:Experimental source: stigma, style; strain Petit Havana SRI  
 C:Genetics:  
 A:Gene: CELP-2  
 C:Superfamily: glutelin  
 C:Keywords: cell wall; extracellular matrix; fertilization  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-196/Product: cysteine-rich extensin-like protein 2 #status experimental <MAT>

Query Match 50.0%; Score 51.5; DB 2; Length 196;  
 Best Local Similarity 43.8%; Pred. No. 6.3;

Matches 7; Conservative 1; Mismatches 1; Indels 7; Gaps 1;

QY 4 WPM-----WPMKP 12  
 ||| ||: ||  
 DB 40 WPMETPCYLTWPFPM 55

## RESULT 12

cysteine-rich extensin-like protein 1 precursor - common tobacco  
 C:Species: Nicotiana tabacum (common tobacco)  
 C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 01-Dec-2000  
 C:Accession: A48233; PQ0475; S24617  
 R:Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993  
 A:Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain  
 A:Reference number: A48233; MUID:93342083  
 A:Accession: A48232  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-209 <WUA>  
 A:Cross-references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923  
 R:de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.  
 Plant Cell 4, 1041-1051, 1992  
 A:Title: Developmental expression of tobacco pistil-specific genes encoding novel extensin  
 A:Reference number: PQ0474; MUID:93005740  
 A:Accession: PQ0475  
 A:Molecule type: mRNA  
 A:Residues: 39-209 <GOL>  
 A:Cross-references: EMBL:Z14020; NID:g19918; PID:g19919  
 A:Experimental source: stigma, style; strain Petit Havana SRI  
 C:Superfamily: glutelin  
 C:Keywords: cell wall; extracellular matrix; fertilization; glycoprotein  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-209/Product: cysteine-rich extensin-like protein 1 #status experimental <MAT>  
 F:146/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 50.0%; Score 51.5; DB 2; Length 209;  
 Best Local Similarity 43.8%; Pred. No. 6.7;  
 Matches 7; Conservative 1; Mismatches 1; Indels 7; Gaps 1;

QY 4 WPM-----WPMKP 12  
 ||| ||: ||  
 DB 45 WPMETPCYLTWPFPM 60

## RESULT 13

photosynthetic reaction center chain L, terbutryn-resistant - Rubrivivax gelatinosus  
 C:Species: Rubrivivax gelatinosus  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
 C:Accession: S68239  
 R:Ouchane, S.; Picard, M.; Astier, C.  
 FEBS Lett. 374, 130-134, 1995  
 A:Title: A new mutation in the pufL gene responsible for the terbutryn resistance phe  
 A:Reference number: S68239; MUID:96049571  
 A:Accession: S68239  
 A:Molecule type: DNA  
 A:Residues: 1-279 <OUC>  
 A:Cross-references: EMBL:U03010; NID:g927301; PIDN:AAA73927.1; PID:g927302  
 A:Experimental source: strain 1  
 C:Genetics:  
 A:Gene: pufL  
 C:Superfamily: reaction center protein  
 C:Keywords: photosynthesis; transmembrane protein

Query Match 50.0%; Score 51.5; DB 2; Length 279;  
 Best Local Similarity 40.9%; Pred. No. 8.9;

Matches 9; Conservative 2; Mismatches 2; Indels 9; Gaps 2;

QY 1 SRRWP-WMPW-----KWPL 13  
 :||| ||: ||  
 DB 257 TRGMPWMMWMLNLPWQWPL 278

## RESULT 14

photosynthetic reaction center complex L subunit, PufL - Rhodocyclus gelatinosus  
 C:Species: Rhodocyclus gelatinosus  
 C:Date: 06-Oct-1994 #sequence\_revision 19-Jul-1996 #text\_change 16-Feb-1997  
 C:Accession: E49964  
 R:Nagashima, K.V.; Matsura, K.; Ohyama, S.; Shimada, K.  
 J. Biol. Chem. 269, 2477-2484, 1994  
 A:Title: Primary structure and transcription of genes encoding B870 and photosynthetic  
 A:Reference number: A49964; MUID:94132007  
 A:Accession: E49964  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-279 <NAG>  
 A:Note: sequence extracted from NCBI backbone (NCBIN:143423, NCBI:143428)  
 A:Note: source designated as Rubrivivax gelatinosus  
 C:Superfamily: reaction center protein

Query Match 50.0%; Score 51.5; DB 2; Length 279;  
 Best Local Similarity 40.9%; Pred. No. 8.9;  
 Matches 9; Conservative 2; Mismatches 2; Indels 9; Gaps 2;

QY 1 SRRWP-WMPW-----KWPL 13  
 :||| ||: ||  
 DB 257 TRGMPWMMWMLNLPWQWPL 278

## RESULT 15

photosynthetic reaction center complex chain L [imported] - Rubrivivax gelatinosus  
 C:Species: Rubrivivax gelatinosus  
 C:Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 28-Jul-2000  
 C:Accession: T50889  
 R:Nagashima, K.V.; Igarashi, N.; Hatada, J.; Nagashima, S.; Matsura, K.; Shimada, K.  
 submitted to the EMBL Data Library, November 1999  
 A:Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photos

A:Reference number: Z25270  
A:Accession: T50889  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-279 <NAG>  
A:Cross-references: EMBL:AB034704; PIDN:BAA94042.1  
A:Experimental source: strain IL144  
C:Genetics:  
A:Gene: pufl  
C:Superfamily: reaction center protein

Query Match 50.0%; Score 51.5; DB 2; Length 279;  
Best local Similarity 40.9%; Pred. No. 8.9;  
Matches 9; Conservative 2; Mismatches 2; Indels 9; Gaps 2;

QY 1 SRRWP-WMPW-----KWPL 13  
: | | | | : | |  
Db 257 TRGWPEWGWMLNLPISQWPL 278

Search completed: January 30, 2002, 11:50:30  
Job time: 124 sec

